-- CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a continuing application of co-pending International Patent Application PCT/US98/16879, filed August 13, 1998, which is a continuation-in-part of United States provisional patent application 60/055,772, filed August 13, 1997. --.

Page 10, line 5, delete " is colored blue, domain 2 red, and domain 3 green. The sulfate and DNA are colored in yellow.", and substitute therefor -- is located at the top left portion of the molecule containing a seventh β-strand running antiparallel to the rest of the sheet, domain 2 is located at the top right portion, domain 3 which is predominantly α-helical is situated at the bottom portion of the molecule. The DNA that is bound in the center of the molecule and the sulfate which is bound to domain 1 are also shown.--

Page 10, line 8, delete "(blue)" and "(red)".

Page 10, line 17, delete "orange color depicts" and substitute therefor -- bright and thick lines depict --; line 19, delete "blue color depicts" and substitute therefor -- faint and thin lines depict --.

Page 54, line 12, delete "Δ", and substitute therefor -- Å --.

IN THE CLAIMS

In claim 11, step a., page 100, after "NS3" insert -- helicase --.

In claim 15, page 103, delete "Δ", and substitute therefor -- Å --.

In claim 18, page 105, delete "Δ", and substitute therefor -- Å --.

In claim 21, step a., page 107, delete "U8" and substitute therefor -- U4 --.

In claim 22, page 108, delete "Δ", and substitute therefor -- Å --; in step a. delete "U8" and substitute therefor -- NTP --.

In claim 24, page 109, after "electron density map of" insert -- at least a portion

A3 of --.

14. (Amended) A method for evaluating the potential of a chemical entity to associate with:

A4 a) a molecule or molecular complex comprising a binding pocket defined by structure coordinates of NS3 helicase amino acids Val232, Thr254, Gly255, Thr269, Gly271, Lys272, Ala275, Trp501 and Tyr502 according to Figure 1, or

b) a homologue of said molecule or molecular complex, wherein said homologue comprises a binding pocket that has a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 [Δ] Å comprising the steps of:

I) employing computational means to perform a fitting operation between the chemical entity and a binding pocket of the molecule or molecular complex; [and]

ii) analyzing the results of said fitting operation to quantify the association between the chemical entity and the binding pocket[.]; and

iii) outputting said quantified association to a suitable output hardware.

16. (Amended) A method for evaluating the potential of a chemical entity to associate with:

A5 a) a molecule or molecular complex comprising a binding pocket defined by structure coordinates of NS3 helicase amino acids His369, Ser370, Lys371, Tyr392, Arg393, Thr411, Asp412, Ala413, Cys431, Val432, Gln434, Ile446, Thr448, Arg461, Glu493, Glu555, Asn556 and Phe557 according to Figure 1, or

b) a homologue of said molecule or molecular complex, wherein said homologue comprises a binding pocket that has a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å comprising the steps of:

I) employing computational means to perform a fitting operation between the chemical entity and a binding pocket of the molecule or molecular complex; [and]

ii) analyzing the results of said fitting operation to quantify the association between the chemical entity and the binding pocket[.]; and

iii) outputting said quantified association to a suitable output hardware.

17. (Amended) A method for evaluating the potential of a chemical entity to associate with:

a) a molecule or molecular complex comprising a binding pocket defined by structure coordinates of NS3 helicase amino acids Pro205, Thr206, Gly207, Ser208, Gly209, Lys210, Ser211, Thr212, Lys213, Asn229, Ala234, Gly237, Phe238, Tyr241, Asp290, Glu291, His293, Thr322, Ala323, Thr324, Gln460, Gly463, Arg464 and Arg467 according to Figure 1, or

b) a homologue of said molecule or molecular complex, wherein said homologue comprises a binding pocket that has a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å comprising the steps of:

I) employing computational means to perform a fitting operation between the chemical entity and a binding pocket of the molecule or molecular complex; [and]

ii) analyzing the results of said fitting operation to quantify the association between the chemical entity and the binding pocket[.]; and

iii) outputting said quantified association to a suitable output hardware.